



## SEQUENCE LISTING

<110> Rieping, Mechthild

<120> A process for producing L-amino acids using strains of the  
Enterobacteriaceae family

<130> 7909/81000

<140> US/10/812,315

<141> 2004-03-30

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 32

<212> DNA

<213> Artificial

<220>

<223> PCR Primer

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<211> 25

<212> DNA

<213> Artificial

<220>

<223> PCR Primer

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<210> 3<211> 1446

<212> DNA

<213> Escherichia coli

<220>

<221> DNA fragment

<222> (1)..(1446)

<223> PCR product

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<221> CDS

<222> (33)..(1427)

<223> galP coding region

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ggg cgg tca aac aag gca atg acg ttt ttc gtc tgc ttc ctt gcc gct 101  
Gly Arg Ser Asn Lys Ala Met Thr Phe Phe Val Cys Phe Leu Ala Ala  
10 15 20

ctg gcg gga tta ctc ttt ggc ctg gat atc ggt gta att gct ggc gca 149  
Leu Ala Gly Leu Leu Phe Gly Leu Asp Ile Gly Val Ile Ala Gly Ala  
25 30 35

ctg ccg ttt att gca gat gaa ttc cag att act tcg cac acg caa gaa Leu Pro Phe Ile Ala Asp Glu Phe Gln Ile Thr Ser His Thr Gln Glu 40 45 50 55	197
tgg gtc gta agc tcc atg atg ttc ggt gcg gca gtc ggt gcg gtg ggc Trp Val Val Ser Ser Met Met Phe Gly Ala Ala Val Gly Ala Val Gly 60 65 70	245
agc ggc tgg ctc tcc ttt aaa ctc ggg cgc aaa aag agc ctg atg atc Ser Gly Trp Leu Ser Phe Lys Leu Gly Arg Lys Lys Ser Leu Met Ile 75 80 85	293
ggc gca att ttg ttt gtt gcc ggt tcg ctg ttc tct gcg gct gcg cca Gly Ala Ile Leu Phe Val Ala Gly Ser Leu Phe Ser Ala Ala Ala Pro 90 95 100	341
aac gtt gaa gta ctg att ctt tcc cgc gtt cta ctg ggg ctg gcg gtg Asn Val Glu Val Leu Ile Leu Ser Arg Val Leu Leu Gly Leu Ala Val 105 110 115	389
ggc gtc gcc tct tat acc gca cgc ctg tac ctc tct gaa att gcg ccg Gly Val Ala Ser Tyr Thr Ala Pro Leu Tyr Leu Ser Glu Ile Ala Pro 120 125 130 135	437
gaa aaa att cgt ggc agt atg atc tcg atg tat cag ttg atg atc act Glu Lys Ile Arg Gly Ser Met Ile Ser Met Tyr Gln Leu Met Ile Thr 140 145 150	485
atc ggc atc ctc ggt gct tat ctt tct gat acc gcc ttc agc tac acc Ile Gly Ile Leu Gly Ala Tyr Leu Ser Asp Thr Ala Phe Ser Tyr Thr 155 160 165	533
ggc gca tgg cgc tgg atg ctg ggt gtg att atc atc ccg gca att ttg Gly Ala Trp Arg Trp Met Leu Gly Val Ile Ile Ile Pro Ala Ile Leu 170 175 180	581
ctg ctg att ggt gtc ttc ttc ctg cca gac agc cca cgt tgg ttt gcc Leu Leu Ile Gly Val Phe Phe Leu Pro Asp Ser Pro Arg Trp Phe Ala 185 190 195	629
gcc aaa cgc cgt ttt gtt gat gcc gaa cgc gtg ctg cta cgc ctg cgt Ala Lys Arg Arg Phe Val Asp Ala Glu Arg Val Leu Leu Arg Leu Arg 200 205 210 215	677
gac acc agc gcg gaa gcg aaa cgc gaa ctg gat gaa atc cgt gaa agt Asp Thr Ser Ala Glu Ala Lys Arg Glu Leu Asp Glu Ile Arg Glu Ser 220 225 230	725
ttg cag gtt aaa cag agt ggc tgg gcg ctg ttt aaa gag aac agc aac Leu Gln Val Lys Gln Ser Gly Trp Ala Leu Phe Lys Glu Asn Ser Asn 235 240 245	773
ttc cgc cgc gcg gtg ttc ctt ggc gta ctg ttg cag gta atg cag caa Phe Arg Arg Ala Val Phe Leu Gly Val Leu Leu Gln Val Met Gln Gln 250 255 260	821
ttc acc ggc atg aac gtc atc atg tat tac gcg ccg aaa atc ttc gaa Phe Thr Gly Met Asn Val Ile Met Tyr Tyr Ala Pro Lys Ile Phe Glu 265 270 275	869
ctg gcg ggt tat acc aac act acc gag caa atg tgg ggc acc gtg att Leu Ala Gly Tyr Thr Asn Thr Thr Glu Gln Met Trp Gly Thr Val Ile 280 285 290 295	917

gtc ggc ctg acc aac gta ctt gcc acc ttt atc gca atc ggc ctt gtt 965  
 Val Gly Leu Thr Asn Val Leu Ala Thr Phe Ile Ala Ile Gly Leu Val  
 300 305 310  
 gac cgc tgg gga cgt aaa cca acg cta acg ctg ggc ttc ctg gtg atg 1013  
 Asp Arg Trp Gly Arg Lys Pro Thr Leu Thr Leu Gly Phe Leu Val Met  
 315 320 325  
 gct gct ggc atg ggc gta ctc ggt aca atg atg cat atc ggt att cac 1061  
 Ala Ala Gly Met Gly Val Leu Gly Thr Met Met His Ile Gly Ile His  
 330 335 340  
 tct ccg tcg gcg cag tat ttc gcc atc gcc atg ctg ctg atg ttt att 1109  
 Ser Pro Ser Ala Gln Tyr Phe Ala Ile Ala Met Leu Leu Met Phe Ile  
 345 350 355  
 gtc ggt ttt gcc atg agt gcc ggt ccg ctg att tgg gta ctg tgc tcc 1157  
 Val Gly Phe Ala Met Ser Ala Gly Pro Leu Ile Trp Val Leu Cys Ser  
 360 365 370 375  
 gaa att cag ccg ctg aaa ggc cgc gat ttt ggc atc acc tgc tcc act 1205  
 Glu Ile Gln Pro Leu Lys Gly Arg Asp Phe Gly Ile Thr Cys Ser Thr  
 380 385 390  
 gcc acc aac tgg att gcc aac atg atc gtt ggc gca acg ttc ctg acc 1253  
 Ala Thr Asn Trp Ile Ala Asn Met Ile Val Gly Ala Thr Phe Leu Thr  
 395 400 405  
 atg ctc aac acg ctg ggt aac gcc aac acc ttc tgg gtg tat gcg gct 1301  
 Met Leu Asn Thr Leu Gly Asn Ala Asn Thr Phe Trp Val Tyr Ala Ala  
 410 415 420  
 ctg aac gta ctg ttt atc ctg ctg aca ttg tgg ctg gta ccg gaa acc 1349  
 Leu Asn Val Leu Phe Ile Leu Leu Thr Leu Trp Leu Val Pro Glu Thr  
 425 430 435  
 aaa cac gtt tcg ctg gaa cat att gaa cgt aat ctg atg aaa ggt cgt 1397  
 Lys His Val Ser Leu Glu His Ile Glu Arg Asn Leu Met Lys Gly Arg  
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 aaa ctg cgc gaa ata ggc gct cac gat taa tctccccaag cttcctccc 1446  
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 Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln  
 35 40 45  
 Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly  
 50 55 60  
 Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly  
 65 70 75 80

Arg	Lys	Lys	Ser	Leu	Met	Ile	Gly	Ala	Ile	Leu	Phe	Val	Ala	Gly	Ser	
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Leu	Phe	Ser	Ala	Ala	Ala	Pro	Asn	Val	Glu	Val	Leu	Ile	Leu	Ser	Arg	
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Val	Leu	Leu	Gly	Leu	Ala	Val	Gly	Val	Ala	Ser	Tyr	Thr	Ala	Pro	Leu	
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Tyr	Leu	Ser	Glu	Ile	Ala	Pro	Glu	Lys	Ile	Arg	Gly	Ser	Met	Ile	Ser	
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Met	Tyr	Gln	Leu	Met	Ile	Thr	Ile	Gly	Ile	Leu	Gly	Ala	Tyr	Leu	Ser	
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Ile	Ile	Ile	Pro	Ala	Ile	Leu	Leu	Leu	Ile	Gly	Val	Phe	Phe	Leu	Pro	
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Asp	Ser	Pro	Arg	Trp	Phe	Ala	Ala	Lys	Arg	Arg	Phe	Val	Asp	Ala	Glu	
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Leu	Leu	Gln	Val	Met	Gln	Gln	Phe	Thr	Gly	Met	Asn	Val	Ile	Met	Tyr	
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Tyr	Ala	Pro	Lys	Ile	Phe	Glu	Leu	Ala	Gly	Tyr	Thr	Asn	Thr	Thr	Glu	
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Thr	Leu	Gly	Phe	Leu	Val	Met	Ala	Ala	Gly	Met	Gly	Val	Leu	Gly	Thr	
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Met	Met	His	Ile	Gly	Ile	His	Ser	Pro	Ser	Ala	Gln	Tyr	Phe	Ala	Ile	
			340					345					350			
Ala	Met	Leu	Leu	Met	Phe	Ile	Val	Gly	Phe	Ala	Met	Ser	Ala	Gly	Pro	
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Phe	Gly	Ile	Thr	Cys	Ser	Thr	Ala	Thr	Asn	Trp	Ile	Ala	Asn	Met	Ile	
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Leu Trp Leu Val Pro Glu Thr Lys His Val Ser Leu Glu His Ile Glu  
435 440 445

Arg Asn Leu Met Lys Gly Arg Lys Leu Arg Glu Ile Gly Ala His Asp  
450 455 460